PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/716,169C*

1644

DATE: 03/25/98
TIME: 17:12:19

INPUT SET: S24411.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

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 1                              SEQUENCE LISTING
 2
 3    (1)     General Information:
 4    (i)   APPLICANT: ANDERTON, STEPHEN MARK
 5                     VAN DER ZEE, RUURD
 6                     VAN EDEN, WILLEM
 7    (ii)   TITLE OF INVENTION: PEPTIDE FRAGMENTS OF MICROBIAL STRESS
 8    PROTEINS AND PHARMACEUTICAL COMPOSITION MADE THEREOF FOR THE
 9    TREATMENT AND PREVENTION OF INFLAMMATORY DISEASES
10    (iii) NUMBER OF SEQUENCES: 6
11    (iv) CORRESPONDENCE ADDRESS:
12    (A) ADDRESSEE: THE WEBB LAW FIRM
13    (B) STREET: 700 KOPPERS BUILDING, 436 SEVENTH AVENUE
14    (C) CITY: PITTSBURGH
15    (D) STATE: PENNSYLVANIA
16    (E) COUNTRY: UNITED STATES OF AMERICA
17    (F) ZIP: 15219-1818
18    (v) COMPUTER READABLE FORM:
19    (A) MEDIUM TYPE: 3.5" FLOPPY DISK
20    (B) COMPUTER: DIGITAL VENTURIS GL 6200
21    (C) OPERATING SYSTEM: DOS
22    (D) SOFTWARE: MICROSOFT WORD 2.0c
23    (vi) CURRENT APPLICATION DATA:
24    (A) APPLICATION NUMBER: 08/716,169
25    (B) FILING DATE: 18-SEP-1996
26    (C) CLASSIFICATION:
27    (vii) PRIOR APPLICATION DATA:
28    (A) APPLICATION NUMBER: PCT/NL95/00108
29    (B) FILING DATE: 21-MAR-1995
30    (2) INFORMATION FOR SEQ ID NO: 1:
31    (i) SEQUENCE CHARACTERISTICS:
32    (A) LENGTH: 540
33    (B) TYPE: AMINO ACID
34    (C) STRANDEDNESS: SINGLE
35    (D) TOPOLOGY: UNKNOWN
36    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
37    Met Ala Lys Thr Ile Ala Tyr Asp Glu Glu Ala Arg Arg Gly Leu
38    1               5                   10                  15
39
40    Glu Arg Gly Leu Asn Ala Leu Ala Asp Ala Val Lys Val Thr Leu
41                    20                  25                  30
42
43    Gly Pro Lys Gly Arg Asn Val Val Leu Glu Lys Lys Trp Gly Ala
44                    35                  40                  45
45
46    Pro Thr Ile Thr Asn Asp Gly Val Ser Ile Ala Lys Glu Ile Glu
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INPUT SET: S24411.raw

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47                    50                    55                    60
48
49   Leu Glu Asp Pro Tyr Glu Lys Ile Gly Ala Glu Leu Val Lys Glu
50                    65                    70                    75
51
52   Val Ala Lys Lys Thr Asp Asp Val Ala Gly Asp Gly Thr Thr Thr
53                    80                    85                    90
54
55   Ala Thr Val Leu Ala Gln Ala Leu Val Arg Glu Gly Leu Arg Asn
56                    95                    100                   105
57
58   Val Ala Ala Gly Ala Asn Pro Leu Gly Val Lys Arg Gly Ile Glu
59                    110                   115                   120
60
61   Lys Ala Val Glu Lys Val Thr Glu Thr Leu Leu Lys Gly Ala Lys
62                    125                   130                   135
63
64   Glu Val Glu Thr Lys Glu Gln Ile Ala Ala Thr Ala Ala Ile Ser
65                    140                   145                   150
66
67   Ala Gly Asp Gln Ser Ile Gly Asp Leu Ile Ala Glu Ala Met Asp
68                    155                   160                   165
69
70   Lys Val Gly Asn Glu Gly Val Ile Thr Val Glu Glu Ser Asn Thr
71                    170                   175                   180
72
73   Phe Gly Leu Gln Leu Glu Leu Thr Glu Gly Met Arg Phe Asp Lys
74                    185                   190                   195
75
76   Gly Tyr Ile Ser Gly Tyr Phe Val Thr Asp Pro Glu Arg Gln Glu
77                    200                   205                   210
78
79   Ala Val Leu Glu Asp Pro Tyr Ile Leu Leu Val Ser Ser Lys Val
80                    215                   220                   225
81
82   Ser Thr Val Lys Asp Leu Leu Pro Leu Leu Glu Lys Val Ile Gly
83                    230                   235                   240
84
85   Ala Gly Lys Pro Leu Leu Ile Ile Ala Glu Asp Val Glu Gly Glu
86                    245                   250                   255
87
88   Ala Leu Ser Thr Leu Val Val Asn Lys Ile Arg Gly Thr Phe Lys
89                    260                   265                   270
90
91   Ser Val Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala
92                    275                   280                   285
93
94   Met Leu Gln Asp Met Ala Ile Leu Thr Gly Gly Gln Val Ile Ser
95                    290                   295                   300
96
97   Glu Glu Val Gly Leu Thr Leu Glu Asn Ala Asp Leu Ser Leu Leu
98                    305                   310                   315
99
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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/716,169C*

INPUT SET: S24411.raw

```
100   Gly Lys Ala Arg Lys Val Val Val Thr Lys Asp Glu Thr Thr Ile
101               320             325                     330
102
103   Val Glu Gly Ala Gly Asp Thr Asp Ala Ile Ala Gly Arg Val Ala
104               335             340                     345
105
106   Gln Ile Arg Gln Glu Ile Glu Asn Ser Asp Ser Asp Tyr Asp Arg
107               350             355                     360
108
109   Glu Lys Leu Gln Glu Arg Leu Ala Lys Leu Ala Gly Gly Val Ala
110               365             370                     375
111
112   Val Ile Lys Ala Gly Ala Ala Thr Glu Val Glu Leu Lys Glu Arg
113               380             385                     390
114
115   Lys His Arg Ile Glu Asp Ala Val Arg Asn Ala Lys Ala Ala Val
116               395             400                     405
117
118   Glu Glu Gly Ile Val Ala Gly Gly Gly Val Thr Leu Leu Gln Ala
119               410             415                     420
120
121   Ala Pro Thr Leu Asp Glu Leu Lys Leu Glu Gly Asp Glu Ala Thr
122               425             430                     435
123
124   Gly Ala Asn Ile Val Lys Val Ala Leu Glu Ala Pro Leu Lys Gln
125               440             445                     450
126
127   Ile Ala Phe Asn Ser Gly Leu Glu Pro Gly Val Val Ala Glu Lys
128               455             460                     465
129
130   Val Arg Asn Leu Pro Ala Gly His Gly Leu Asn Ala Gln Thr Gly
131               470             475                     480
132
133   Val Lys Glu Asp Leu Leu Ala Ala Gly Val Ala Asp Pro Val Lys
134               485             490                     495
135
136   Val Thr Arg Ser Ala Leu Gln Asn Ala Ala Ser Ile Ala Gly Leu
137               500             505                     510
138
139   Phe Leu Thr Thr Glu Ala Val Val Ala Asp Lys Pro Glu Lys Glu
140               515             520                     525
141
142   Lys Ala Ser Val Pro Gly Gly Gly Asp Met Gly Gly Met Asp Phe
143               530             535                     540
144
145   (2) INFORMATION FOR SEQ ID NO: 2:
146   (i) SEQUENCE CHARACTERISTICS:
147   (A) LENGTH: 333
148   (B) TYPE: AMINO ACID
149   (C) STRANDEDNESS: SINGLE
150   (D) TOPOLOGY: UNKNOWN
151   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
152   Ala Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Asn
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INPUT SET: S24411.raw

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153   1                 5                      10                     15
154
155   Val Phe Arg Ala Ala Leu Lys Asn Pro Asp Ile Glu Val Val Ala
156                    20                     25                     30
157
158   Val Asn Asp Leu Thr Asp Ala Asn Thr Leu Ala His Leu Leu Lys
159                    35                     40                     45
160
161   Tyr Asp Ser Val His Gly Arg Leu Asp Ala Glu Val Ser Val Asn
162                   ·50                     55                     60
163
164   Gly Asn Asn Leu Val Val Asn Gly Lys Glu Ile Ile Val Lys Ala
165                    65                     70                     75
166
167   Glu Arg Asp Pro Glu Asn Leu Ala Trp Gly Glu Ile Gly Val Asp
168                    80                     85                     90
169
170   Ile Val Val Glu Ser Thr Gly Arg Phe Thr Lys Arg Glu Asp Ala
171                    95                    100                    105
172
173   Ala Lys His Leu Glu Ala Gly Ala Lys Lys Val Ile Ile Ser Ala
174                   110                    115                    120
175
176   Pro Ala Lys Asn Glu Asp Ile Thr Ile Val Met Gly Val Asn Gln
177                   125                    130                    135
178
179   Asp Lys Tyr Asp Pro Lys Ala His His Val Ile Ser Asn Ala Ser
180                   140                    145                    150
181
182   Cys Thr Thr Asn Cys Leu Ala Pro Phe Ala Lys Val Leu His Glu
183                   155                    160                    165
184
185   Gln Phe Gly Ile Val Arg Gly Met Met Thr Thr Val His Ser Tyr
186                   170                    175                    180
187
188   Thr Asn Asp Gln Arg Ile Leu Asp Leu Pro His Lys Asp Leu Arg
189                   185                    190                    195
190
191   Arg Ala Arg Ala Ala Ala Glu Ser Ile Ile Pro Thr Thr Thr Gly
192                   200                    205                    210
193
194   Ala Ala Lys Ala Val Ala Leu Val Leu Pro Glu Leu Lys Gly Lys
195                   215                    220                    225
196
197   Leu Asn Gly Met Ala Met Arg Val Pro Thr Pro Asn Val Ser Val
198                   230                    235                    240
199
200   Val Asp Leu Val Ala Glu Leu Glu Lys Glu Val Thr Val Glu Glu
201                   245                    250                    255
202
203   Val Asn Ala Ala Leu Lys Ala Ala Ala Glu Gly Glu Leu Lys Gly
204                   260                    265                    270
205
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206   Ile Leu Ala Tyr Ser Glu Glu Pro Leu Val Ser Arg Asp Tyr Asn
207                   275              280              285
208
209   Gly Ser Thr Val Ser Ser Thr Ile Asp Ala Leu Ser Thr Met Val
210                   290              295              300
211
212   Ile Asp Gly Lys Met Val Lys Val Val Ser Trp Tyr Asp Asn Glu
213                   305              310              315
214
215   Thr Gly Tyr Ser His Arg Val Val Asp Leu Ala Ala Tyr Ile Ala
216                   320              325              330
217
218   Ser Lys Gly
219
220   (2) INFORMATION FOR SEQ ID NO: 3:
221   (i) SEQUENCE CHARACTERISTICS:
222   (A) LENGTH: 332
223   (B) TYPE: AMINO ACID
224   (C) STRANDEDNESS: SINGLE
225   (D) TOPOLOGY: UNKNOWN
226   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
227   Val Lys Val Gly Val Asn Gly Phe Gly Arg Ile Gly Arg Leu Val
228   1               5                10               15
229
230   Thr Arg Ala Ala Phe Ser Cys Asp Lys Val Asp Ile Val Ala Ile
231                   20               25               30
232
233   Asn Asp Pro Phe Ile Asp Leu Asn Tyr Met Val Tyr Met Phe Gln
234                   35               40               45
235
236   Tyr Asp Ser Thr His Gly Lys Phe Asn Gly Thr Val Lys Ala Glu
237                   50               55               60
238
239   Asn Gly Lys Leu Val Ile Asn Gly Lys Pro Ile Thr Ile Phe Gln
240                   65               70               75
241
242   Glu Arg Asp Pro Val Lys Ile Lys Trp Gly Asp Ala Gly Ala Glu
243                   80               85               90
244
245   Tyr Val Val Glu Ser Thr Gly Val Phe Thr Thr Met Glu Lys Ala
246                   95               100              105
247
248   Gly Ala His Leu Lys Gly Gly Ala Lys Arg Val Ile Ile Ser Ala
249                   110              115              120
250
251   Pro Ser Ala Asp Ala Pro Met Phe Val Met Gly Val Asn His Glu
252                   125              130              135
253
254   Lys Tyr Asp Asn Ser Leu Lys Ile Val Ser Asn Ala Ser Cys Thr
255                   140              145              150
256
257   Thr Asn Cys Leu Ala Pro Leu Ala Lys Val Ile His Asp Asn Phe
258                   155              160              165
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/716,169C*

INPUT SET: S24411.raw

Line	Error	Original Text